



## Protein families database of alignments and HMMs

|                      |                                |                                |                             |                            |                          |                     |                   |
|----------------------|--------------------------------|--------------------------------|-----------------------------|----------------------------|--------------------------|---------------------|-------------------|
| <a href="#">Home</a> | <a href="#">Keyword Search</a> | <a href="#">Protein Search</a> | <a href="#">Browse Pfam</a> | <a href="#">DNA Search</a> | <a href="#">Taxonomy</a> | <a href="#">ftp</a> | <a href="#">H</a> |
|----------------------|--------------------------------|--------------------------------|-----------------------------|----------------------------|--------------------------|---------------------|-------------------|

UBA



**Figure 1: 1aip**  
**C complex of two elongation factors**  
 Ef-tu ef-ts complex from thermus  
 thermophilus

### Key:

| D main                      | Chain | Start Residue | End Residue |
|-----------------------------|-------|---------------|-------------|
| <a href="#">GTP_EFTU_D3</a> | A     | 309           | 404         |
| <a href="#">GTP_EFTU_D2</a> | A     | 235           | 305         |
| <a href="#">GTP_EFTU</a>    | A     | 9             | 214         |
| <a href="#">GTP_EFTU_D3</a> | B     | 309           | 404         |
| <a href="#">GTP_EFTU_D2</a> | B     | 235           | 305         |
| <a href="#">GTP_EFTU</a>    | B     | 9             | 214         |
| <a href="#">UBA</a>         | C     | 2             | 42          |
| <a href="#">EF_TS</a>       | C     | 55            | 196         |
| <a href="#">UBA</a>         | D     | 2             | 42          |
| <a href="#">EF_TS</a>       | D     | 55            | 196         |
| <a href="#">GTP_EFTU_D3</a> | E     | 309           | 404         |
| <a href="#">GTP_EFTU_D2</a> | E     | 235           | 305         |
| <a href="#">GTP_EFTU</a>    | E     | 9             | 214         |
| <a href="#">GTP_EFTU_D3</a> | F     | 309           | 404         |
| <a href="#">GTP_EFTU_D2</a> | F     | 235           | 305         |
| <a href="#">GTP_EFTU</a>    | F     | 9             | 214         |
| <a href="#">UBA</a>         | G     | 2             | 42          |
| <a href="#">EF_TS</a>       | G     | 55            | 196         |
| <a href="#">UBA</a>         | H     | 3             | 42          |
| <a href="#">EF_TS</a>       | H     | 55            | 196         |

The Swissprot/PDB mapping was provided by [MSD](#)

**Accession number:** PF00627

### UBA/TS-N domain

[Add Annotation](#)

This small domain is composed of three alpha helices. This family includes the previously defined UBA and TS-N domains. The UBA-domain (ubiquitin associated domain) is a novel sequence motif found in several proteins having connections to ubiquitin and the ubiquitination pathway. The structure of the UBA domain consists of a compact three helix bundle [1]. This domain is found at the N terminus of EF-TS hence the name TS-N. The structure of EF-TS is known and this domain is implicated in its interaction with EF-TU [2]. The domain has been found in non EF-TS proteins such as alpha-NAC [P70670](#) and MJ0280 [Y280\\_METJA](#) [1].

This family forms **structural complexes** with other Pfam families, to view them click [here](#)

### INTERPRO description (entry IPR000449)

UBA domains are a commonly occurring sequence motif of approximately 45 amino acid residues that are found in diverse proteins involved in the ubiquitin/proteasome pathway, DNA excision-repair, and cell signaling via protein kinases [[MEDLINE:97025177](#)]. The human homologue of yeast Rad23A is one example of a nucleotide excision-repair protein that contains both an internal and a C-terminal UBA domain.

The solution structure of human Rad23A UBA(2) showed that the domain forms a compact three-helix bundle [[MEDLINE:99061330](#)]. Comparison of the structures of UBA(1) and UBA(2) reveals that both form very similar folds and have a conserved large hydrophobic surface patch which may be a common protein-interacting surface present in diverse UBA domains. Evidence that ubiquitin binds to UBA domains leads to the prediction that the hydrophobic surface patch of UBA domains interacts with the hydrophobic surface on the five-stranded  $\beta$ -sheet of ubiquitin [[MEDLINE:22075341](#)].

|   |             |
|---|-------------|
| 1dv0 ▾  | Display pdb |
| For additional annotation, see the <a href="#">PROSITE</a> document PDOC50015 [ <a href="#">Expasy</a>   <a href="#">SRS-UK</a>   <a href="#">SRS-USA</a> ] |             |

| Alignment  | Domain organisation  |
|--|--|
| <input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528)<br>Format <span>Coloured alignment ▾</span><br><div> <a href="#">Get alignment</a> <a href="#">View HMM logo</a> </div> Further alignment options <a href="#">here</a><br>Help relating to Pfam alignments <a href="#">here</a> | <input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528) <input type="radio"/> Context (58)<br><div> <div> <b>As a Graphic</b><br/>           Zoom <span>0.5</span> pixels/aa. <input type="checkbox"/> Bootstrap tree<br/> <a href="#">View Graphic</a> </div> <div> <b>As a Tree</b><br/> <a href="#">NIFAS Applet</a> </div> </div> To find out about the NIFAS tree-viewer, click <a href="#">here</a> |
| Species Distribution   | Phylogenetic tree  |
| <b>NEW!</b> View alignments & domain organisation by species<br>Tree depth: <span>Show all levels ▾</span><br><a href="#">View Species Tree</a>  | <input checked="" type="radio"/> Seed (162) <input type="radio"/> Full (528)<br><div> <a href="#">Download tree</a> <a href="#">ATV Applet</a> </div> The trees were generated using Quicktree<br>To find out more about ATV phylogenetic tree-viewer click <a href="#">here</a>   |

| Database References  |  |
|--|--|
| <b>PDB</b><br>You can find out how to set up Rasmol <a href="#">here</a> | <div>1dv0 A; 1; 40; ▾</div> <div> <a href="#">PDB; 2 Pfam</a> <a href="#">Scop Cath Pfam</a> </div> <div> <a href="#">CATH-PDBSUM</a> <a href="#">SCOP-UK</a> </div>         |
| <b>PROSITE</b>   | PD0C50015 [ <a href="#">Expasy</a>   <a href="#">SRS-UK</a>   <a href="#">SRS-USA</a> ]  |
| <b>URL</b>   | <a href="http://www.isrec.isb-sib.ch/profile/isrec96/poster.html">http://www.isrec.isb-sib.ch/profile/isrec96/poster.html</a>  |
| <b>PROSITE_PROFILE</b>   | PS50030  |
| <b>HOMSTRAD</b>  | EF_TS  |
| <b>PFAMB</b>   | <a href="#">PB009949</a> <a href="#">PB014089</a> <a href="#">PB027029</a> <a href="#">PB047420</a> <a href="#">PB054475</a> <a href="#">PB092955</a> <a href="#">PB0940</a> |
| <b>SYSTERS</b>   | <a href="#">UBA</a>  |
| <b>PANDIT</b>  | <a href="#">UBA</a>  |

| Literature References  | Pfam specific information |           |
|--|---------------------------|-----------|
| 1.<br><b>The structure of the Escherichia coli EF-Tu.EF-Ts complex at 2.5 Å resolution.</b><br>Kawashima T, Berthet-Colominas C, Wulff M, Cusack S, Leberman R; Nature 1996;379:511-518. | Author of entry           | Bateman A |
|  | Type definition           | Domain    |
|  | Alignment method of seed  | Manual    |
|  | Source of seed members    | Bateman A |

**2.**

**Structure of a human DNA repair protein UBA domain that interacts with HIV-1 Vpr.**

Dieckmann T, Withers-Ward ES, Jarosinski MA, Liu CF, Chen IS, Feigon J;  
Nat Struct Biol 1998;5:1042-1047.

**3. Alignment of TS-N domain is in figure 7c.**

**Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell.**

Makarova KS, Aravind L, Galperin MY, Grishin NV, Tatusov RL, Wolf YI, Koonin EV;  
Genome Res 1999;9:608-628.

**HMMER build information**

|                     | <b>Pfam_ls</b> [ <a href="#">Download HMM</a> ]         | <b>Pfam_fs</b> [ <a href="#">Download HMM</a> ]            |
|---------------------|---|--|
| Gathering cutoff    | 17.3 17.3;  | 19.0 19.0  |
| Trusted cutoff      | 17.3 17.3;  | 19.0 19.0  |
| Noise cutoff        | 17.2 17.2;  | 18.9 18.9  |
| Build method of HMM | hmmbuild -F HMM_ls SEED<br>hmmcalibrate --seed 0 HMM_ls | hmmbuild -f -F HMM_fs SEED<br>hmmcalibrate --seed 0 HMM_fs |

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